

**\*10049710\*****PCT10****RAW SEQUENCE LISTING**

DATE: 01/04/2003

PATENT APPLICATION: **US/10/049,710A**

TIME: 20:49:11

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1 <110> APPLICANT: Shinmyo, Atsuhiko  
2 Kato, Kou  
3 Yamada, Yasuhiro  
4 Nihira, Takuya  
5 Shindo, Takuya  
6 <120> TITLE OF INVENTION: METHOD FOR INDUCTION OF GENE EXPRESSION IN PLANT AND PLANT  
TREATED  
7 THEREBY  
8 <130> FILE REFERENCE: 5405/18  
C--> 9 <140> **CURRENT APPLICATION NUMBER: US/10/049,710A**  
10 <141> CURRENT FILING DATE: 2002-02-15  
11 <150> PRIOR APPLICATION NUMBER: PCT/JP01/05096  
12 <151> PRIOR FILING DATE: 2001-06-15  
13 <150> PRIOR APPLICATION NUMBER: JP 2000-180466  
14 <151> PRIOR FILING DATE: 2000-06-15  
15 <160> NUMBER OF SEQ ID NOS: 11  
16 <170> SOFTWARE: PatentIn version 3.1  
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19 <211> LENGTH: 699  
20 <212> TYPE: DNA  
21 <213> ORGANISM: Streptomyces virginiae  
22 <220> FEATURE:  
23 <221> NAME/KEY: CDS  
24 <222> LOCATION: (1)..(699)  
25 <223> OTHER INFORMATION:  
26 <300> PUBLICATION INFORMATION:  
27 <301> AUTHORS: Okamoto, S., Nakamura, K., Nihira, T. and Yamada, Y.  
28 <302> TITLE: Virginiae butanolide binding protein from Streptomyces virginiae.  
29 Evidence that VbrA is not the virginiae butanolide binding protein and re-  
30 identification of the true binding protein  
31 <303> JOURNAL: Journal of Biological Chemistry  
32 <304> VOLUME: 270  
33 <305> ISSUE: 20  
34 <306> PAGES: 12319-12326  
35 <307> DATE: 1995-05-19  
36 <308> DATABASE ACCESSION NO: D32251  
37 <309> DATABASE ENTRY DATE: 1994-07-19  
38 <313> RELEVANT RESIDUES: (1)..(699)  
39 <300> PUBLICATION INFORMATION:  
40 <301> AUTHORS: Okamoto, S., Nakamura, K., Nihira, T. and Yamada, Y.  
41 <302> TITLE: Virginiae butanolide binding protein from Streptomyces virginiae.  
42 Evidence that VbrA is not the virginiae butanolide binding protein and re-  
43 identification of the true binding protein

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44 <303> JOURNAL: Journal of Biological Chemistry

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 55 cgc acg cgg cag gcg atc gtg cgg gca gcc gcc tcg gtc ttc gac gag 96  
 56 Arg Thr Arg Gln Ala Ile Val Arg Ala Ala Ala Ser Val Phe Asp Glu  
 57 20 25 30  
 58 tac ggg ttc gag gcc gcc aca gtg gca gag atc ctc tcg cgg gcc tcg 144  
 59 Tyr Gly Phe Glu Ala Ala Thr Val Ala Glu Ile Leu Ser Arg Ala Ser  
 60 35 40 45  
 61 gtc acc aag ggc gcg atg tac ttc cac ttc gct tcc aag gaa gag ctg 192  
 62 Val Thr Lys Gly Ala Met Tyr Phe His Phe Ala Ser Lys Glu Glu Leu  
 63 50 55 60  
 64 gcc cgc ggc gtg ctg gcc gag cag acc ctg cac gtg gcg gtg ccg gaa 240  
 65 Ala Arg Gly Val Leu Ala Glu Gln Thr Leu His Val Ala Val Pro Glu  
 66 65 70 75 80  
 67 tcc ggc tcc aag gcg cag gaa ctg gta gac ctc acc atg ctg gtc gcc 288  
 68 Ser Gly Ser Lys Ala Gln Glu Leu Val Asp Leu Thr Met Leu Val Ala  
 69 85 90 95  
 70 cac ggc atg ctg cac gat ccg atc ctg cgg gcg ggc acg cgg ctc gca 336  
 71 His Gly Met Leu His Asp Pro Ile Leu Arg Ala Gly Thr Arg Leu Ala  
 72 100 105 110  
 73 ctg gac cag ggg gcg gtg gac ttc tcc gac gcc aac ccg ttc ggc gag 384  
 74 Leu Asp Gln Gly Ala Val Asp Phe Ser Asp Ala Asn Pro Phe Gly Glu  
 75 115 120 125  
 76 tgg ggc gac atc tgc gcc cag ctc ctg gcg gag gca cag gaa cgg ggg 432  
 77 Trp Gly Asp Ile Cys Ala Gln Leu Leu Ala Glu Ala Gln Glu Arg Gly  
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 80 Glu Val Leu Pro His Val Asn Pro Lys Lys Thr Gly Asp Phe Ile Val  
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 83 Gly Cys Phe Thr Gly Leu Gln Ala Val Ser Arg Val Thr Ser Asp Arg  
 84 165 170 175  
 85 cag gac ctc ggc cac cgg atc tcg gtg atg tgg aac cac gtg ctg ccc 576  
 86 Gln Asp Leu Gly His Arg Ile Ser Val Met Trp Asn His Val Leu Pro  
 87 180 185 190  
 88 agc atc gtg ccg gcg tcc atg ctg acc tgg atc gaa acc ggc gag gag 624  
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 90 195 200 205  
 91 cgg atc ggg aag gtc gcg gcg gcg gcc gag gcc gcc gag gct gcg gag 672  
 92 Arg Ile Gly Lys Val Ala Ala Ala Glu Ala Ala Glu Ala Ala Glu  
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 107 Tyr Gly Phe Glu Ala Ala Thr Val Ala Glu Ile Leu Ser Arg Ala Ser  
 108 35 40 45  
 109 Val Thr Lys Gly Ala Met Tyr Phe His Phe Ala Ser Lys Glu Glu Leu  
 110 50 55 60  
 111 Ala Arg Gly Val Leu Ala Glu Gln Thr Leu His Val Ala Val Pro Glu  
 112 65 70 75 80  
 113 Ser Gly Ser Lys Ala Gln Glu Leu Val Asp Leu Thr Met Leu Val Ala  
 114 85 90 95  
 115 His Gly Met Leu His Asp Pro Ile Leu Arg Ala Gly Thr Arg Leu Ala  
 116 100 105 110  
 117 Leu Asp Gln Gly Ala Val Asp Phe Ser Asp Ala Asn Pro Phe Gly Glu  
 118 115 120 125  
 119 Trp Gly Asp Ile Cys Ala Gln Leu Leu Ala Glu Ala Gln Glu Arg Gly  
 120 130 135 140  
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 122 145 150 155 160  
 123 Gly Cys Phe Thr Gly Leu Gln Ala Val Ser Arg Val Thr Ser Asp Arg  
 124 165 170 175  
 125 Gln Asp Leu Gly His Arg Ile Ser Val Met Trp Asn His Val Leu Pro  
 126 180 185 190  
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 135 <211> LENGTH: 26  
 136 <212> TYPE: DNA  
 137 <213> ORGANISM: Streptomyces virginiae  
 138 <300> PUBLICATION INFORMATION:  
 139 <301> AUTHORs: Kinoshita, H., Tsuji, T., Ipposhi, H., Nihira, T. and Yamada, Y.  
 140 <302> TITLE: Characterization of Binding Sequences for Butyrolactone Autoregulator  
 141 Receptors in Streptomyces  
 142 <303> JOURNAL: Journal of Bacteriology  
 143 <304> VOLUME: 181  
 144 <305> ISSUE: 16

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150 <300> PUBLICATION INFORMATION:
151 <301> AUTHORS: Kinoshita, H., Tsuji, T., Ipposhi, H., Nihira, T. and Yamada, Y.
152 <302> TITLE: Characterization of Binding Sequences for Butyrolactone Autoregulator
153      Receptors in Streptomyces
154 <303> JOURNAL: Journal of Bacteriology
155 <304> VOLUME: 181
156 <305> ISSUE: 16
157 <306> PAGES: 5075-5080
158 <307> DATE: 1999-08
159 <308> DATABASE ACCESSION NO: D32251
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169 <223> OTHER INFORMATION: Designed sequence of the CamV 35S promoter modified to
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170      operator BARE-3 element just downstream of its TAT-box
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179 <220> FEATURE:
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181      operator BARE-3 element just upstream of its TATA-box
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183      gatattctcca ctgacgtaag g gatgacgca caatcagata cataccaacc ggttcttttg      60
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214 <223> OTHER INFORMATION: Designed sequence of a backward primer containing the
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215     enzyme BamH I recognition sequence for PCR amplification of the barA gene
216     coding region to be cloned by cut with the enzyme
217 <400> SEQUENCE: 8
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224 <220> FEATURE:
225 <223> OTHER INFORMATION: Designed sequence of a forward primer containing the
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226     enzyme Sac I recognition sequence for PCR amplification of the barA gene
227     coding region to be cloned by cut with the enzyme
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234 <213> ORGANISM: Artificial sequence
235 <220> FEATURE:
236 <223> OTHER INFORMATION: Designed sequence of one of paired oligo DNAs for
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237     modified CaMV 35S promoter containing three of the operator BARE-3 elements
238     just downstream and upstream of its TATA-box
239 <400> SEQUENCE: 10
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241     tgactat                                          67
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245 <212> TYPE: DNA
246 <213> ORGANISM: Artificial sequence
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248 <223> OTHER INFORMATION: Designed sequence of the other of paired oligo DNAs for
construction
249     of the modified CaMV 35S promoter containing three of the operator BARE-3

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